A●Monta

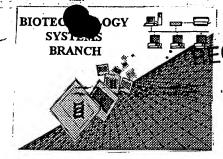# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/331,723_

Source: _1638_

Date Processed by STIC: _11-07-00_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

[ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

[ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

[X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

[ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

[ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

[ ] 7. Other: _____

Applicant Must Provide:

[X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

[ ] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
    Technical Assistance......................................703-287-0200
    To Purchase PatentIn Software.......................703-306-2600

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A.mehta

RAW SEQUENCE LISTING   DATE: 11/07/2000
PATENT APPLICATION: US/09/331,723   TIME: 11:47:54

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11072000\I331723.raw

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 3 <110> APPLICANT: BOYNTON, John
 4       GILLHAM, Nicholas
 5       RANDOLPH-ANDERSON, Barbara
 6       ISHIGE, Fumiharu
 7       SATO, Ryo
 9 <120> TITLE OF INVENTION: METHODS OF CONFERRING PPO-INHIBITING HERBICIDE RESISTANCE IN PLANTS BY
10       GENE MANIPULATION
12 <130> FILE REFERENCE: 2185-156P
14 <140> CURRENT APPLICATION NUMBER: US 09/331,723
15 <141> CURRENT FILING DATE: 1999-08-18
17 <150> PRIOR APPLICATION NUMBER: PCT/US96/20415
18 <151> PRIOR FILING DATE: 1996-12-27
20 <160> NUMBER OF SEQ ID NOS: 24
22 <170> SOFTWARE: PatentIn version 3.0
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26 <212> TYPE: PRT
27 <213> ORGANISM: Chlamydomonas reinhardtii
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30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: ()..()
32 <223> OTHER INFORMATION: Strain CC-407
35 <220> FEATURE:
36 <221> NAME/KEY: PEPTIDE
37 <222> LOCATION: (1)..(47)
38 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain
41 <400> SEQUENCE: 1
43 Ala Ala Glu Ala Leu Gly Ser Phe Asp Tyr Pro Pro Val Gly Ala Val
44 1               5                   10                  15
46 Thr Leu Ser Tyr Pro Leu Ser Ala Val Arg Glu Glu Arg Lys Ala Ser
47               20                  25                  30
49 Asp Gly Ser Val Pro Gly Phe Gly Gln Leu His Pro Arg Thr Gln
50           35                  40                  45
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 46
54 <212> TYPE: PRT
55 <213> ORGANISM: Arabidopsis thaliana
57 <220> FEATURE:
58 <221> NAME/KEY: misc_feature
59 <222> LOCATION: ()..()
60 <223> OTHER INFORMATION: ecotype Columbia
63 <220> FEATURE:
64 <221> NAME/KEY: PEPTIDE
65 <222> LOCATION: (1)..(46)
66 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain
69 <400> SEQUENCE: 2
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74 Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
75             20            25            30
77 Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln
78         35             40             45
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81 <211> LENGTH: 46
82 <212> TYPE: PRT
83 <213> ORGANISM: Zea mays
85 <220> FEATURE:
86 <221> NAME/KEY: misc_feature
87 <222> LOCATION: ()..()
88 <223> OTHER INFORMATION: Strain B73 inbred
91 <220> FEATURE:
92 <221> NAME/KEY: PEPTIDE
93 <222> LOCATION: (1)..(46)
94 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain
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100 1             5             10             15
102 Thr Val Ser Tyr Pro Lys Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp
103         20            25             30
105 Gly Glu Leu Gln Gly Phe Gly Gln Leu His Pro Arg Ser Gln
106         35             40             45
108 <210> SEQ ID NO: 4
109 <211> LENGTH: 141
110 <212> TYPE: DNA
111 <213> ORGANISM: Chlamydomonas reinhardtii
113 <220> FEATURE:
114 <221> NAME/KEY: misc_feature
115 <222> LOCATION: ()..()
116 <223> OTHER INFORMATION: Strain CC-407
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120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(141)
122 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
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128 ccgctgagcg ccgtgcggga ggagcgcaag gcctcggacg ggtccgtgcc gggcttcggt     120
130 cagctgcacc cgcgcacgca g                                              141
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134 <211> LENGTH: 138
135 <212> TYPE: DNA
136 <213> ORGANISM: Arabidopsis thaliana
138 <220> FEATURE:
139 <221> NAME/KEY: misc_feature
140 <222> LOCATION: ()..()
141 <223> OTHER INFORMATION: ecotype Columbia
144 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 11/07/2000
PATENT APPLICATION: US/09/331,723   TIME: 11:47:54

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\11072000\I331723.raw**

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147 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
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153 ccgaaagaag caatccgaac agaatgtttg atagatggtg aactaaaggg ttttgggcaa     120
155 ttgcatccac gcacgcaa                                                   138
158 <210> SEQ ID NO: 6
159 <211> LENGTH: 138
160 <212> TYPE: DNA
161 <213> ORGANISM: Zea mays
163 <220> FEATURE:
164 <221> NAME/KEY: misc_feature
165 <222> LOCATION: ()..()
166 <223> OTHER INFORMATION: Strain B73 inbred
169 <220> FEATURE:
170 <221> NAME/KEY: misc_feature
171 <222> LOCATION: (1)..(138)
172 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
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178 ccaaaggaag caattagaaa agaatgctta attgatgggg aactccaggg ctttggccag     120
180 ttgcatccac gtagtcaa                                                   138
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184 <211> LENGTH: 36
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
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189 <221> NAME/KEY: misc_feature
190 <222> LOCATION: (1)..(36)
191 <223> OTHER INFORMATION: Oligonucleotide primer for Arabidopsis thaliana
194 <400> SEQUENCE: 7
195 ctatattacc caccaatggc agcagtatct atctcg                               36
198 <210> SEQ ID NO: 8
199 <211> LENGTH: 38
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <221> NAME/KEY: misc_feature
205 <222> LOCATION: (1)..(38)
206 <223> OTHER INFORMATION: Oligonucleotide primer for Zea mays
209 <400> SEQUENCE: 8
210 gattctatta tccaccgatg gctgctgtaa ctgtttcg                             38
213 <210> SEQ ID NO: 9
214 <211> LENGTH: 26
215 <212> TYPE: PRT
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <221> NAME/KEY: misc_feature
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RAW SEQUENCE LISTING DATE: 11/07/2000
PATENT APPLICATION: US/09/331,723 TIME: 11:47:54

Input Set : A:\PTO.txt
Output Set: N:\CRF3\11072000\I331723.raw
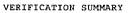
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220 <222> LOCATION: ()..()
221 <223> OTHER INFORMATION: Oligonucleotide primer common to both of A. thaliana and Z. mays
222      p
225 <220> FEATURE:
226 <221> NAME/KEY: misc_feature
227 <222> LOCATION: ()..()
228 <223> OTHER INFORMATION: "n" residues can be inosine in addition to G, A, T or C; "k" at p
229      o
232 <400> SEQUENCE: 9
234 Lys Ala Tyr Thr Ala Tyr Cys Cys Asn Cys Cys Asn Ala Thr Gly Gly
235 1           5               10              15
237 Ser Asn Gly Cys Asn Gly Thr Asn Trp Ser
238             20              25
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241 <211> LENGTH: 2573
242 <212> TYPE: DNA
243 <213> ORGANISM: Chlamydomonas reinhardtii
245 <220> FEATURE:
246 <221> NAME/KEY: misc_feature
247 <222> LOCATION: ()..()
248 <223> OTHER INFORMATION: Strain RS-3
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252 <221> NAME/KEY: misc_feature
253 <222> LOCATION: (1)..(2573)
254 <223> OTHER INFORMATION: encodes protoporphyrinogen oxidase
257 <400> SEQUENCE: 10
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260 acgtccccct ttcctgctac ccgctccccc ccggctttac tgccccttcc actcctcggc   120
262 tccatcccga ttccatccgc tcctcctccc ccacctagac tgtctaccgt ctaccagttt   180
264 cttgggcaat cattaacgta acccgcctc cctgcgcctg cccctccctc cctctccccc    240
266 ccgcacagcc cgccgccgcc gaggccctgg gctccttcga ctaccggcg atgggcgccg    300
268 tgacgctgtc gtaccgctg agcgccgtgc gggaggagcg caaggcctcg gacgggtccg    360
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272 gcggtgtgtt gcggagggga gggtggtggg ggttggggt gggggtgggg gggattgggg    480
274 cgctgggtcg tatcccgcgg ttgtatcctc gcgctcccct catccattcc ccccttcaac   540
276 aacacacacg ggcgcacacg caccctcttt gcgcttactt tgtctggtgc tccttaacac   600
278 actcttcgct tcattttggt gtcttctaac acacacactt gtccacacac agggcatcac   660
280 cactctgggc accatctaca gctccagcct gttccccggc cgcgcgcccg agggccacat   720
282 gctgctgctc aactacatcg gcggcaccac caaccgcggc atcgtcaacc agaccaccga   780
284 gcagctggtg gagcaggtgt gtgtgtgggg gggtggggg ggggcagtgg atttttgggc    840
286 tgagcccccct gagcaaagcg atccagggg ggcgaagccc cccaggattg ccctgtccg    900
288 tgcgtgcgtg tgtgcctgtg tcgacaaaaa gtaccgtact ggcacaaacc gcgagtgcca   960
290 cgtattatta attgcaatta cctattgtag aaaaatagac ggcagggaaa actcggccgg  1020
292 agcgagaagc gacctcgtga gtccatggac atcttgactt tcttcagttc gcgagtatag  1080
294 ctctcggccc ctaaatatct tacatccatg tatcaaaaca tgtcgacgac aagcgtcttg  1140
296 gggcaagaat gtcgaaattg tttgcaacag ccaaaccatg cgtccccgag ccttacatgt  1200
298 gtcgcggccc gggatcccgc gcccgagccc ggctagccct ttgcggtgct tgagtgggat  1260
300 gtgggtgagg tgcatttggg atatcatgga ccgtgaagtg gcgtgggtaa ggtggcgtgg  1320
302 cgtggcgggg acagggcatg tcggtgcctc ggcacagcgt tggcctagtg gccagtcccg  1380
```

?

This is an amino acid sequence.

```
304 ctggatgggc ttgcaagggt gctgttcatg tcgccggtgc ccatcgtcac atccccttgc   1440
306 gctacatggg gctcagccca ttttccagct gtacaaagct gacacccctt gttgtgtggc   1500
308 gtcttggacc cgtgttgctt cggagctggc cagaaccccc tgtgggcaca cacacgcaca   1560
310 cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca   1620
312 cacacacaca cacacacaca cacacacaca cacacacaca cacattttcg tcctgcagcc   1680
314 ccgaaccccg ccgcccgttc cacgtcttcc acctgccgca cccccccccc tgccgcacgc   1740
316 ctgctctcac cgcctctccc cccacccccat ctccctgcag gtgaacaagg acctgcgcaa   1800
318 catggtcatc aagcccgacg cgcccaagcc ccgtgtggtg ggcgtgcgcg tgtggccgcg   1860
320 cgccatcccg caggtgtgag ggcgcagcag ccggagggat gggctagatc ctagtttctc   1920
322 aaagagctct acagccctat aacctcgacc tgcgaccttc gacctgataa cctggctgcc   1980
324 ccctcccaac ctagccacct ctccccggat ttgggttcac tcggttgact tgcttttggg   2040
326 ttctggaatc aacttcacct gttgtatact ttgctgcact tctctgtacc actctttgca   2100
328 ttaggttcgg tttagtttgg gctgcatgtg taacccctcc tccccgccct gccacctgca   2160
330 gttcaacctg ggccacctgg agcagctgga caaggcgcgc aaggcgctgg acgcggcggg   2220
332 gctgcagggc gtgcacctgg ggggcaacta cgtcagcggt gagcgcgtgg gcagcagcag   2280
334 cagcaggaag aggggagggg aggggatggg aggtacaag gaggaggttg agcaggaggt   2340
336 ggtgctaagg cgcaaagcaa ggcggtgttg tatcctcatt gactgaaacc gggaaaccca   2400
338 gcatgaacaa gaggtcaggg gactgcaagg agcggaggct acatgtatga ctaccccga   2460
340 cgcqggcgat gattccttga ctattgggac ctatttcgtt gggctcgggc acatgacccc   2520
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345 <210> SEQ ID NO: 11
346 <211> LENGTH: 1704
347 <212> TYPE: DNA
348 <213> ORGANISM: Arabidopsis thaliana
350 <220> FEATURE:
351 <221> NAME/KEY: misc_feature
352 <222> LOCATION: ()..()
353 <223> OTHER INFORMATION: ecotype Columbia
356 <220> FEATURE:
357 <221> NAME/KEY: CDS
358 <222> LOCATION: (16)..(1629)
359 <223> OTHER INFORMATION: product = protoporphyrinogen oxidase
362 <400> SEQUENCE: 11
363 ttctctgcga tttcc atg gag tta tct ctt ctc cgt ccg acg act caa tcg      51
364                   Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser
365                    1               5                  10
367 ctt ctt ccg tcg ttt tcg aag ccc aat ctc cga tta aat gtt tat aag      99
368 Leu Leu Pro Ser Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys
369         15                  20                  25
371 cct ctt aga ctc cgt tgt tca gtg gcc ggt gga cca acc gtc gga tct     147
372 Pro Leu Arg Leu Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser
373         30                  35                  40
375 tca aaa atc gaa ggc gga gga ggc acc acc atc acg acg gat tgt gtg     195
376 Ser Lys Ile Glu Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val
377 45                  50                  55                  60
379 att gtc ggc gga ggt att agt ggt ctt tgc atc gct cag gcg ctt gct     243
380 Ile Val Gly Gly Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala
381                     65                  70                  75
383 act aag cat cct gat gct gct ccg aat tta att gtg acc gag gct aag     291
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VERIFICATION SUMMARY   DATE: 11/07/2000
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